

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2006, 11:28:39 ; Search time 1101 Seconds
(without alignments)
2981.311 Million cell updates/sec

Title: US-10-082-018A-2

Perfect score: 1088
Sequence: 1 gcagactcccttcgtaat.....caccaccaccactact 1088

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 6709644 seqs, 1508466879 residues

Total number of hits satisfying chosen parameters: 13419288

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Pending Patents_NA_New: *
1: /SIDS5/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /SIDS5/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /SIDS5/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /SIDS5/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /SIDS5/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /SIDS5/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq1:*
8: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq1:*
9: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq1:*
10: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq2:*
11: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq3:*
12: /SIDS5/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	589	54.1	1176	US-11-039-880-6	Sequence 6, Appl1
2	588	54.0	1140	US-11-039-880-4	Sequence 4, Appl1
3	132.2	12.2	3673778	US-10-312-841A-1	Sequence 1, Appl1
4	109.8	10.1	908	US-11-331-032-6574	Sequence 6574, Ap
5	109.4	10.1	2300	US-60-762-056-3594	Sequence 35494, A
6	106.8	9.8	810	US-11-331-032-6400	Sequence 6400, Ap
7	106.8	9.8	1317241	PCT-US06-08981-73	Sequence 73, Appl
8	102.4	9.4	980	US-11-331-032-6399	Sequence 6399, Appl
9	102.4	9.4	1835834	PCT-US06-08981-72	Sequence 72, Appl
10	101	9.3	2540030	PCT-US06-08981-69	Sequence 69, Appl
11	100.2	9.2	988	US-11-331-032-774	Sequence 774, Ap
12	100	9.2	1038	US-11-360-355-15948	Sequence 15948, A
13	99.6	9.2	17265	US-60-740-736-152	Sequence 152, App
14	99	9.1	1971884	PCT-US06-08981-70	Sequence 70, Appl
15	98.6	9.1	899	US-11-353-150-24647	Sequence 24647, A
16	98.6	9.1	1317241	PCT-US06-08981-73	Sequence 73, Appl
17	98	9.0	2300	US-60-762-056-21229	Sequence 21229, A
18	97.2	8.9	777	US-11-331-032-1045	Sequence 1045, Ap
19	96.8	8.9	1202	US-11-360-355-22884	Sequence 22884, A
20	96.6	8.9	607	US-11-331-032-1335	Sequence 1335, Ap
21	95.8	8.8	1099	US-11-331-032-6603	Sequence 6603, Ap

22	95.8	8.8	1836	US-11-360-355-31136	Sequence 31136, A
23	95.8	8.8	3673778	US-10-312-841A-2	Sequence 2, Appl1
24	95.6	8.8	2501	PCT-US04-20336-369	Sequence 369, App
25	95.6	8.8	2501	US-10-506-111-1172	Sequence 172, App
26	95.6	8.8	2501	US-11-317-798-369	Sequence 369, App
27	95.6	8.8	3673778	US-10-312-841A-2	Sequence 2, Appl1
28	95.4	8.8	2540030	PCT-US06-08981-69	Sequence 69, Appl
29	94.2	8.7	17265	US-60-740-736-280	Sequence 280, App
30	94	8.6	2501	PCT-US04-20336-485	Sequence 485, App
31	94	8.6	2501	US-10-506-111-300	Sequence 300, App
32	94	8.6	2501	US-11-317-798-485	Sequence 485, App
33	92.4	8.5	2300	US-60-762-056-26311	Sequence 26311, A
34	92.2	8.5	11222	US-10-506-111-374	Sequence 374, App
35	92.2	8.5	11222	US-10-506-111-246	Sequence 246, App
36	92.2	8.5	1835834	PCT-US06-08981-72	Sequence 72, Appl
37	92	8.5	1971884	PCT-US06-08981-70	Sequence 70, Appl
38	91.8	8.4	576	US-11-331-032-5638	Sequence 5638, Ap
39	91.8	8.4	1097	US-11-331-032-6594	Sequence 6594, Ap
40	90.4	8.3	711	US-11-331-032-1218	Sequence 1218, Ap
41	90.2	8.3	664	US-11-331-032-12583	Sequence 12583, A
42	89.8	8.3	775	US-11-331-032-6337	Sequence 6337, Ap
43	89.6	8.2	706	US-11-331-032-6390	Sequence 6390, Ap
44	89.4	8.2	2300	US-60-762-056-4574	Sequence 4574, Ap
45	89.4	8.2	20420	US-11-375-555-385	Sequence 385, App

ALIGNMENTS

RESULT 1
US-11-039-880-6
Sequence 6, Application US/11039880
GENERAL INFORMATION:
APPLICANT: Lyon, Jeffrey A.
APPLICANT: Angov, Evelina
TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite
FILE REFERENCE: 003/241/SAP
CURRENT FILING DATE: 2006-01-24
PRIOR APPLICATION NUMBER: US/10/057,531
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/264,535
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/347,564
PRIOR FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 6
LENGTH: 1176
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: E. coli expressed P. falciparum MSP-142 (3D7)
US-11-039-880-6
Query Match 54.1%; Score 589; DB 8; Length 1176;
Best Local Similarity 72.7%; Pred. No. 5.8e-104;
Matches 819; Conservative 0; Mismatches 245; Indels 63; Gaps 2;
QY 4 GNACTCTTCGTAATGATTAACATGCTTTTAATGAATGAATGATGAGTTTGA 63
DB 52 GCATATGCTGTCATGATGATATATCCCTCGAGTTTGAATGAATGATGATGATTA 111
QY 64 TATTTAAACCTTTACAGCTGTTTATGAAGTTTAAAAAACAATTAGAAATTAAGCTT 123
DB 112 TATTTAAACCTTTACAGCTGTTTATGAAGTTTAAAAAACAATTAGAAATTAAGCTT 171
QY 124 ATGACATTTAAGTTATGATTAAGATTAATTTAATTCAGATTTATATAACGTGAAT 183
DB 172 TTATCATTTATTTAATTAATTTGAACGATATCTTAATTCAGCTTTAAGAAACAAATAT 231
QY 184 TTCAAAATGTTTATGATGATGATTTAATTCATATTAAGATTTAATCAATCAATATAT 243

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2006, 11:41:11 ; Search time 1446 Seconds
(without alignments)
3004.414 Million cell updates/sec

Title: US-10-082-018a-2

Perfect score: 1088
Sequence: 1 gcagtaacccttcctcgtaat.....caccaccaccaccactaact 1088

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:*
1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/2/pubpna/PCF_NEW_PUB.seq:*
5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	277.4	25.5	279	14	US-11-144-833-3
2	277.4	25.5	342	14	US-11-144-833-6
3	185	17.0	291	14	US-11-144-833-1
4	185	17.0	330	14	US-11-144-833-9
5	185	17.0	354	14	US-11-144-833-4
6	185	17.0	387	14	US-11-144-833-7
7	93	8.5	1230	6	US-09-925-065A-77681
8	93	8.5	1230	9	US-10-301-480-178920
9	93	8.5	1230	10	US-10-301-480-178920
10	93	8.5	1230	14	US-11-121-086-25
11	92.8	8.5	49979	8	US-10-995-561-13443
12	92.8	8.5	979	10	US-10-301-480-595013
13	92.4	8.5	979	10	US-10-301-480-595014
14	92.4	8.5	979	10	US-10-301-480-595015
15	92.4	8.5	979	10	US-10-301-480-1208422
16	92.4	8.5	979	10	US-10-301-480-1208423
17	92.4	8.5	979	10	US-10-301-480-1208424
18	92.4	8.5	980	10	US-10-301-480-595016

19	92.4	8.5	980	10	US-10-301-480-1208425	Sequence 1208425,
20	91.8	8.4	1230	6	US-09-925-065A-77682	Sequence 77682, A
21	91.8	8.4	1230	9	US-10-301-480-178921	Sequence 178921,
22	91.8	8.4	1230	10	US-10-301-480-792330	Sequence 792330,
23	91.4	8.4	1230	6	US-09-925-065A-77683	Sequence 77683, A
24	91.4	8.4	1230	6	US-09-925-065A-77684	Sequence 77684, A
25	91.4	8.4	1230	9	US-10-301-480-178922	Sequence 178922,
26	91.4	8.4	1230	9	US-10-301-480-178923	Sequence 178923,
27	91.4	8.4	1230	10	US-10-301-480-792331	Sequence 792331,
28	91.4	8.4	1230	10	US-10-301-480-792332	Sequence 792332,
29	90.8	8.3	139054	14	US-11-121-086-96	Sequence 96, Appl
30	88	8.1	687411	9	US-10-330-773-26	Sequence 26, Appl
31	84	7.7	26772	8	US-10-995-561-13313	Sequence 13313, A
32	84	7.7	54946	8	US-10-995-561-13479	Sequence 13479, A
33	83.8	7.7	171486	14	US-11-121-086-105	Sequence 105, App
34	83.4	7.7	171486	14	US-11-121-086-105	Sequence 105, App
35	83.2	7.6	173602	14	US-11-121-086-25	Sequence 25, Appl
36	82.2	7.6	139054	14	US-11-121-086-96	Sequence 96, Appl
37	82	7.5	49979	8	US-10-995-561-13443	Sequence 13443, A
38	80	7.4	990	10	US-10-301-480-568794	Sequence 568794,
39	80	7.4	990	10	US-10-301-480-589139	Sequence 589139,
40	79.8	7.3	633	10	US-10-301-480-589140	Sequence 589140,
41	79.8	7.3	633	10	US-10-301-480-1202548	Sequence 1202548,
42	79.8	7.3	633	10	US-10-301-480-1202549	Sequence 1202549,
43	79.8	7.3	633	10	US-10-301-480-1202549	Sequence 1202549,
44	79.4	7.3	5501	8	US-10-240-708-38	Sequence 38, Appl
45	79.2	7.3	990	10	US-10-301-480-568791	Sequence 568791,

ALIGNMENTS

RESULT 1	US-11-144-833-3	Sequence 3, Application US/1144833
1	US-11-144-833-3	Publication No. US20060018932A1
2	US-11-144-833-3	GENERAL INFORMATION:
3	US-11-144-833-3	APPLICANT: LONGACRE-ANDRE, SHIRLEY
4	US-11-144-833-3	APPLICANT: ROTH, CHARLES
5	US-11-144-833-3	APPLICANT: NATO, FARIDABANO
6	US-11-144-833-3	APPLICANT: BARNWELL, JOHN
7	US-11-144-833-3	APPLICANT: MENDIS, KANINI
8	US-11-144-833-3	TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT
9	US-11-144-833-3	TITLE OF INVENTION: OF PLASMODIUM MSP-1
10	US-11-144-833-3	FILE REFERENCE: 0660-0139-0XPC
11	US-11-144-833-3	CURRENT FILING DATE: 2005-06-06
12	US-11-144-833-3	PRIOR FILING DATE: 1997-02-14
13	US-11-144-833-3	PRIOR APPLICATION NUMBER: FR96/01822
14	US-11-144-833-3	PRIOR FILING DATE: 1996-02-14
15	US-11-144-833-3	NUMBER OF SEQ ID NOS: 15
16	US-11-144-833-3	SOFTWARE: Patent version 3.1
17	US-11-144-833-3	SEQ ID NO 3
18	US-11-144-833-3	LENGTH: 279
19	US-11-144-833-3	TYPE: DNA
20	US-11-144-833-3	ORGANISM: Plasmodium falciparum
21	US-11-144-833-3	Query Match
22	US-11-144-833-3	Best Local Similarity 99.6%; Pred. No. 1.1e-27;
23	US-11-144-833-3	Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
24	US-11-144-833-3	DB
25	US-11-144-833-3	787 AACATTTCACACCAACGCTAAACAAATGCGCAAAATTCGATGTTTCAG 846
26	US-11-144-833-3	1 AACATTTCACACCAACGCTAAACAAATGCGCAAAATTCGATGTTTCAG 60
27	US-11-144-833-3	847 CATTAGATGAAGAAGAGATGTAATGTTTAAATTAACAAACAGAGGTGATAA 906
28	US-11-144-833-3	61 CATTAGATGAAGAAGAGATGTAATGTTTAAATTAACAAACAGAGGTGATAA 120

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2006, 10:34:40 ; Search time 4195 Seconds
(without alignments)
12134.528 Million cell updates/sec

Title: US-10-082-018a-2

Sequence: 1 gcagctactcctcgcgtact.....caccaccaccactact 1088

Scoring table: IDENTITY NTC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: EST.*
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2: gb_est2.*
3: gb_est3.*
4: gb_hnc.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gsa1.*
10: gb_gsa2.*
11: gb_gsa3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	384	35.3	606 5 BU496794	BU496794 PESTOab5
2	375.2	34.5	570 5 BU497996	BU497996 PESTOab9
3	339.8	31.2	537 3 BU1815756	BU1815756 PESTOab3
4	310.6	28.5	550 5 BU498549	BU498549 PESTOab9
5	243	22.3	432 5 BU631144	BU631144 PESTOab3
6	230	21.1	419 5 BU451367	BU451367 PESTOab9
7	205.2	18.9	501 3 BU181631	BU181631 PESTOab4
8	204.4	18.8	422 5 BU451709	BU451709 PESTOab0
9	203.4	18.7	365 8 BU452445	BU452445 PESTOab9
10	199.2	18.3	522 5 BU451036	BU451036 PESTOab0
11	198.2	18.2	455 5 BU498112	BU498112 PESTOab9
12	198.2	18.2	476 5 BU670649	BU670649 PESTOab0
13	171	15.7	402 3 BU181539	BU181539 PESTOab1
14	159.2	14.6	303 3 BU181931	BU181931 PESTOab0
15	141.2	13.0	408 5 BU451572	BU451572 PESTOab0
16	141.2	13.0	418 5 BU451661	BU451661 PESTOab0
17	141.2	13.0	422 5 AG349719	AG349719 Mus muscu
18	130	11.9	1254 10 CG757503	CG757503 P052-4-CO
19	129	11.9	1392 10 AG320745	AG320745 Mus muscu
20	125.6	11.5	1612 10 AG347098	AG347098 Mus muscu
21	125.4	11.5	1268 10 AG350209	AG350209 Mus muscu
22	125.4	11.5	1378 10	

23	122.8	11.3	1101	10	CNS008VL	AL069706 Drosophila
24	121.6	11.2	1015	10	CL135318	CL135318 ISB1-106P
25	121	11.1	945	11	CNS040DK	AL285149 Tetradon
26	120.8	11.1	1380	1	AJ928744	AJ928744
27	120.2	11.0	542	3	BM167382	BM167382 EST569905
28	120.2	11.0	964	10	CW957121	CW957121 TCB52.1.C
29	120.2	11.0	1272	1	AJ927522	AJ927522
30	120.2	11.0	1456	10	AG382339	AG382339 Mus muscu
31	119.4	11.0	1536	10	CL078538	CL078538 CH216-151
32	119.2	11.0	1381	10	CL082000	CL082000 CH216-165
33	119	10.9	1260	1	AJ928742	AJ928742
34	119	10.9	1608	10	CL118721	CL118721 ISB1-72J8
35	118.6	10.9	725	3	BM160032	BM160032 EST562555
36	118.2	10.9	1696	10	AG346840	AG346840 Mus muscu
37	118	10.8	1238	1	AJ925855	AJ925855
38	117.4	10.8	1248	8	DN080809	DN080809 73970127
39	117.4	10.8	1594	10	CL038406	CL038406 CH216-46A
40	117	10.8	1348	10	CG749499	CG749499 P043-4-A0
41	116.6	10.7	2157	10	CL081966	CL081966 CH216-165
42	116.4	10.7	1224	10	CL077121	CL077121 CH216-143
43	116.2	10.7	1299	8	DN0709204	DN0709204 CL081-H10
44	115.8	10.6	1626	6	CF238805	CF238805 AGENCOURT
45	115.6	10.6	1260	10	CL491610	CL491610 SAIL_559

ALIGNMENTS

RESULT 1
BU496794
LOCUS
DEFINITION
PESTOab58h11.y1 Plasmodium falciparum 3D7 asexual CDNA Plasmidium falciparum 3D7 CDNA 5' similar to TR:Q9TVG8 Q9TVG8 MSAL PROTEIN ; mRNA Sequence.
ACCESSION
BU496794.1 GI:22792988
VERSION
EST.
SOURCE
Plasmodium falciparum 3D7
ORGANISM
Plasmodium falciparum 3D7
REFERENCE
1 (bases 1 to 606)
Tang,K., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Treising,B., Bowers,T., Gibbons,M., Rletter,E., Bennett,J., Jentle,E., Ronko,I., Teagareishill,L.R., Belaygorod,L., Franklin,C., Carr,L., Grow,A., Maguire,L., Richey,J., Watkins,J., Kennedy,S., Levinso,D., Waterson,R., Wilson,R. and Sibley,D.
AUTHORS
Washu Plasmidium EST Project
TITLE
Washu Plasmidium EST Project
JOURNAL
Contact: L. David Sibley
COMMENT
Unpublished (2001)
Washu Plasmidium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Library was constructed by Debopam Chakrabarti DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: L. David Sibley (lsibley@wustl.edu), Washington University
Seq primer: -400P from G1bco
High quality sequence stop: 428.
Location/Qualifiers
1..606
/organism="Plasmodium falciparum 3D7"
/mol_type="mRNA"
/db_xref="taxon:36329"
/lab_host="DH108 (GeneHog, Invitrogen, Inc.)"
/clone_lib="Plasmodium falciparum 3D7 asexual CDNA"
/notes="Vector: pBluescript SK plus; Site 1: EcoRI, Site 2: XhoI; Library was constructed by Debopam Chakrabarti. Total RNA samples were isolated from mixed stage seponin(0.1%) lysed P. falciparum 3D7 infected

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2006, 10:21:16 ; Search time 5463 Seconds
(without alignments)
11320.826 Million cell updates/sec

Title: US-10-082-018a-2

Sequence: 1 ggaagtaactctctccgtaat.....caccaccaccactact 1088

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sta:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1088	100.0	1088	6	BD072830 Novel mod
2	1088	100.0	1088	6	BD077370 Novel mod
3	1088	100.0	1088	6	CS133015 Sequence
4	1088	100.0	1088	6	AR359785 Sequence
5	1074.8	98.8	1175	6	AR636155 Sequence
6	1065	97.9	1065	2	PFASURPRO
7	1065	97.9	1131	2	AF325919 Plasmodiu
8	1065	97.9	1203	2	PFAMSP1
9	1065	97.9	1636	2	PFAMSP806
10	1065	97.9	1636	2	PFAMSP808
11	1065	97.9	1636	2	PFAMSP837
12	1065	97.9	1636	2	PFAMSP79
13	1065	97.9	1842	6	AR307176 Sequence
14	1065	97.9	1896	6	AR307174 Sequence
15	1065	97.9	1896	6	AR307175 Sequence
16	1065	97.9	1950	6	AR307173 Sequence
17	1065	97.9	4920	6	A92450
18	1065	97.9	5282	2	PFPI90

19	1065	97.9	5917	2	PPANT195	X02919 Plasmodiu
20	1065	97.9	7038	2	PPCP195A	X15063 Plasmodiu
21	1063.4	97.7	1636	2	PFAMSP828	D13360 Plasmodiu
22	1063.4	97.7	1636	2	PFAMSP844	D13363 Plasmodiu
23	1063.4	97.7	1785	6	AR307163	AR307163 Sequence
24	1061.8	97.6	1636	2	PFAMSP8222	D13359 Plasmodiu
25	1061.8	97.6	1636	2	PFAMSP834	D13361 Plasmodiu
26	1005.2	92.4	5760	6	A04562	A04562 P.falciparu
27	1005.2	92.4	5760	6	B00656	B00656 CDNA encodi
28	935.2	86.0	5220	2	AJ786604	AJ786604 Plasmodiu
29	834.2	76.7	1104	11	AY343089	AY343089 Synthetic
30	623.6	57.3	4940	6	A92451	A92451 Sequence 2
31	623.6	57.3	4940	11	CYB131294	AJ131294 Cloning v
32	609.6	56.0	1142	6	BD072836	BD072836 Novel mod
33	609.6	56.0	1142	6	BD077376	BD077376 Novel mod
34	609.6	56.0	1142	6	CS133021	CS133021 Sequence
35	609.6	56.0	1142	6	AR359791	AR359791 Sequence
36	602.8	55.4	1726	2	PFAMSP815	D13346 Plasmodiu
37	602.8	55.4	1726	2	PFAMSP8351	D13348 Plasmodiu
38	602.8	55.4	1726	2	PFAMSP8352	D13349 Plasmodiu
39	602.8	55.4	1726	2	PFAMSP838	D13350 Plasmodiu
40	602.8	55.4	1726	2	PFAMSP842	D13352 Plasmodiu
41	602.8	55.4	1956	2	PFME2SA1D	Z35329 P.falciparu
42	602.8	55.4	5067	2	AB116599	AB116599 Plasmodiu
43	602.8	55.4	5085	2	AF218248	AF218248 Plasmodiu
44	602.8	55.4	5100	2	AB116596	AB116596 Plasmodiu
45	602.8	55.4	5243	2	AF062348	AF062348 Plasmodiu

ALIGNMENTS

RESULT 1	BD072830	1088 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD072830				
DEFINITION	Novel modified MSP-1 nucleic acid sequences and methods for				
ACCESSION	BD072830				
VERSION	BD072830.1	GI:22618433			
KEYWORDS	JP 2001520048-A/2.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 1088)				
AUTHORS	Chang, L.H. and Meade, H.				
TITLE	Novel modified MSP-1 nucleic acid sequences and methods for				
JOURNAL	increasing mRNA levels and protein expressions in cell systems				
GENZYME	Patent: JP 2001520048-A 2 30-OCT-2001;				
RESEARCH	GENZYME TRANSGENICS CORP MAYO FOUNDATION FOR MEDICAL EDUCATION AND				
COMMENT	OS preferable, a bacterium, virus, or parasite				
PN	JP 2001520048-A/2				
PD	30-OCT-2001				
PF	20-OCT-1998 JP 2000517094				
PR	20-OCT-1997 US 60/062592, 15-MAY-1998 US 60/085649 PI				
LI	HOU CHANG, HARRY MEADE				
PC	CI2N15/09, A01K67/027, A61K35/76, A61K39/012, A61K48/00, C07K14/445, PC				
	CI2N1/21.				
CC	CI2N5/10, CI2N15/00, CI2N5/00				
CC	Novel modified MSP-1 nucleic acid sequences and methods for				
CC	increasing				
CC	mRNA levels and protein expressions in cell systems FH Key				
FT	CDS	Location/Qualifiers			
	1..1088	(1)..(1083).			
FEATURES	source	Location/Qualifiers			
	1..1088	Location/Qualifiers			
ORIGIN	1088	Location/Qualifiers			
	1088	Location/Qualifiers			
Query Match	100.0%	Score 1088,	DB 6,	Length 1088,	